

Fig.1

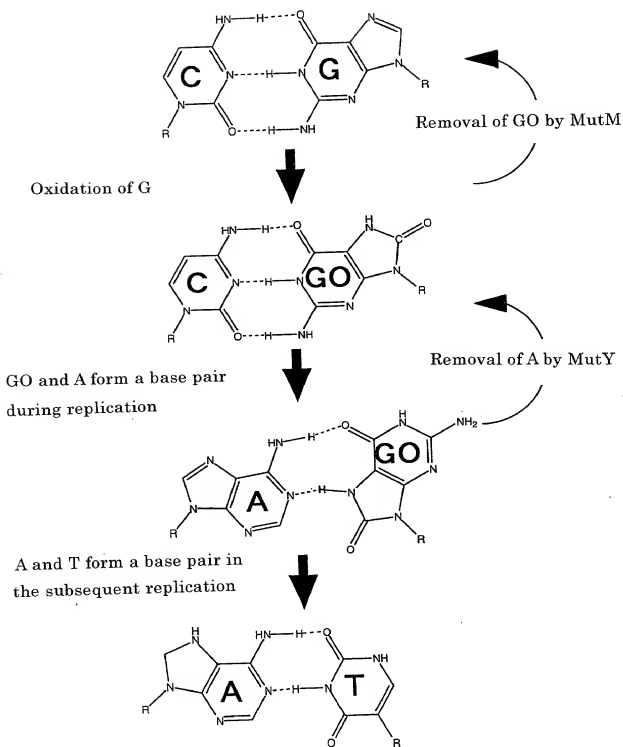


Fig.2

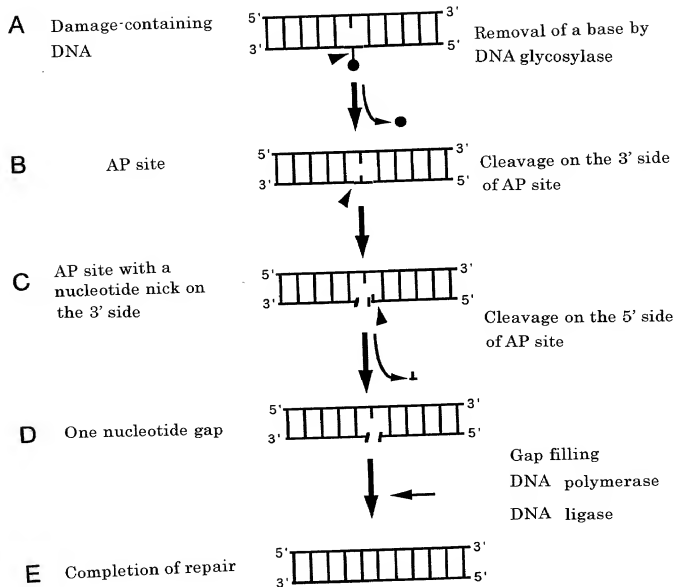


Fig.3

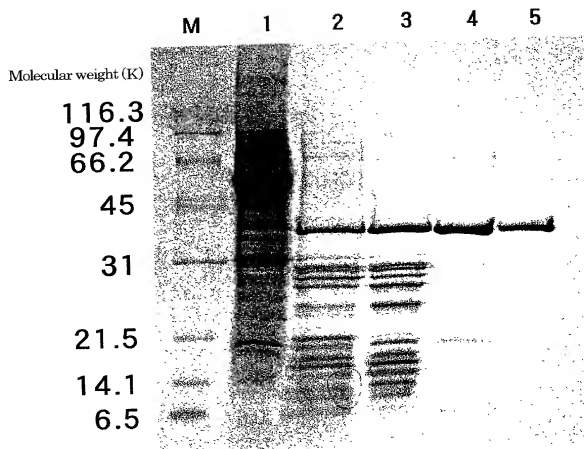


Fig.4

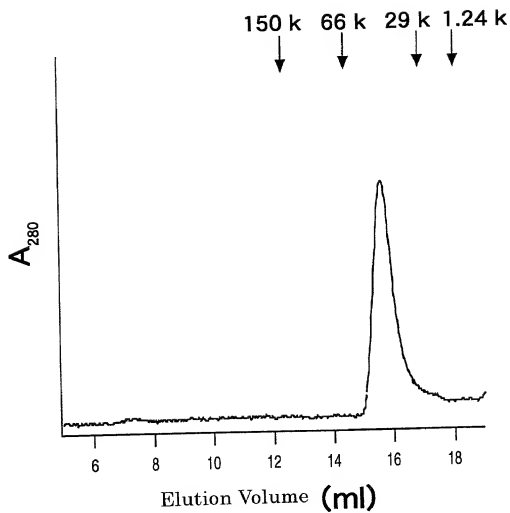


Fig.5

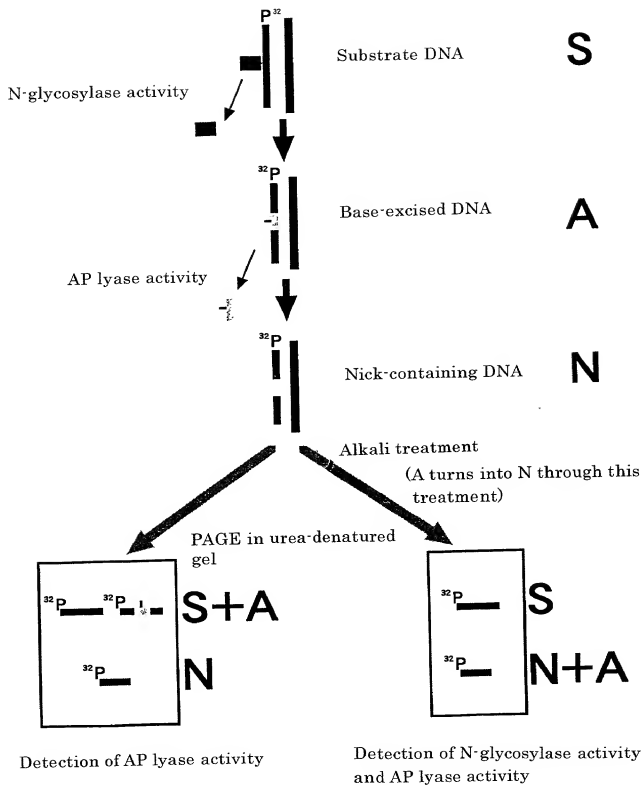
Tth MutY	1	MEAPKAEIA	53	GE	KQYRNISEVLLQOTRVEDALPYRRFL	53
Hsa MutY	51	CDGLARPEEVLQASVSSHLFDVAYTAFRSSK	139	RRAYAWISEVLLQOTVATVINYTGNI	139	
Spo MutY	1	ISDSNHFLLDHYSTOLEVERFSE	86	KTPTKVMILSEVLLQOTVATVIPYFERFI	86	
Eco MutY	1	IQASQFSAGQ	55	FSSPFELL	55	
Eco Endo III	1	MMKAKRELEITLREN	55	ELN	55	
Tth MutY	54	ERTPEKALJACE	145	PSFAELR	145	
Hsa MutY	140	OKMPTDOLLSSE	237	QVETDQLE	237	
Spo MutY	89	ETLETKSCDEVTWMP	187	SLKQHP	187	
Eco MutY	57	APFTVTDLMD	153	THFRVQNTQFAGP	153	
Eco Endo III	56	PVANTPAAMLELOE	153	THFRVQNTQFAGP	153	
Tth MutY	146	PK	210	KEAPGRYP	210	
Hsa MutY	238	DFSTLSVQV	336	EDW	336	
Spo MutY	154	WPKKEIKEN	225	ANNSWALYP	225	
Eco MutY	154	KN	205	EDUCEY	205	
Eco Endo III	154	KN	205	EDUCEY	205	
Tth MutY	211	RRAK	286	GRFAVRS	286	
Hsa MutY	337	OTLGV	425	LPATHLRL	425	
Spo MutY	277	EOLQMMVARYPHFAKTQRE	375	IKKYQSR	375	
Eco MutY	226	QTL	287	IAADNL	287	
Eco Endo III	206	KN	206	IAADNL	206	
Tth MutY	267	GEVRAH	325	AGVPLQIA	325	
Hsa MutY	426	GEVRAH	535	AGVPLQIA	535	
Spo MutY	378	GRYLFHES	461	FKPEPLTSARRI	461	
Eco MutY	288	TAFRHES	350	LLQOLRTGAPV	350	

Tth (*Thermus thermophilus* HB8), Hsa (*Homo sapiens*), Spo (*Schizosaccharomyces pombe*), Eco (*Escherichia coli*)

Residue essential for N-glycosylase activity * Residues constituting an iron-sulfur cluster

(D)

Fig.6



104280*10682660

Fig.7

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21



Fig.8

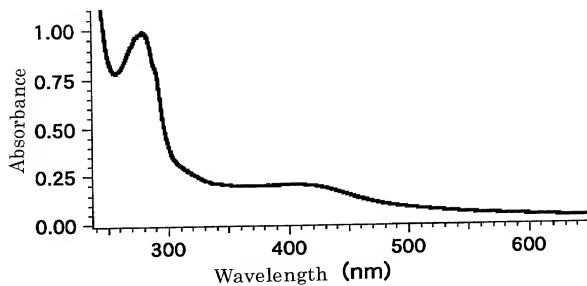


Fig.9

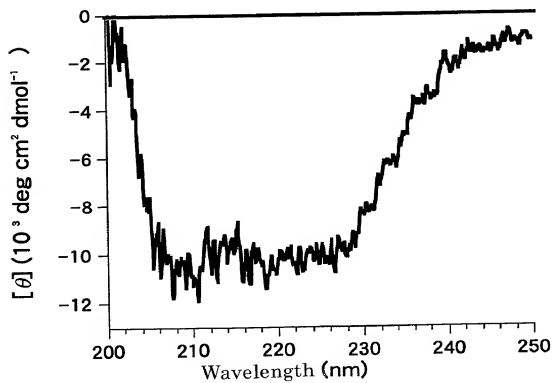


Fig.10

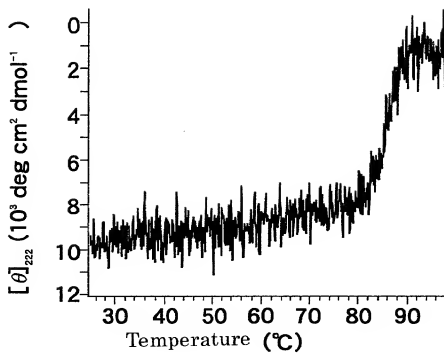


Fig.11

5' -[³²P]AGATCTTGACGGGGAAAYCCGAATTCGGCGAACGTGGCGAG-3'
 3' -AATCTAGAACTGCCCTTTXGGCTTAAGCCGCTTGACCCGCTCTT-5'

X : G, G, C, T

Y : A, G

Annealing

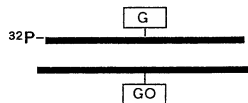
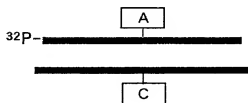
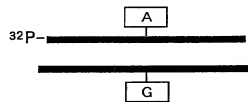
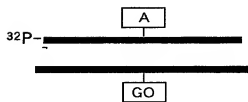


Fig.12

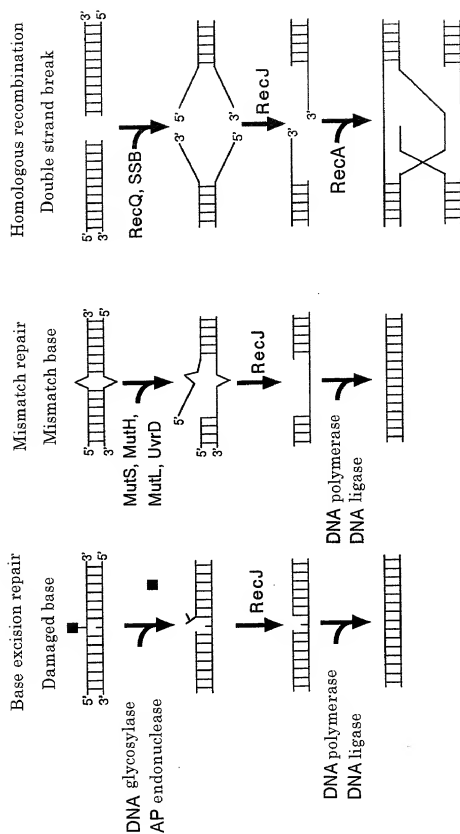


Fig.13

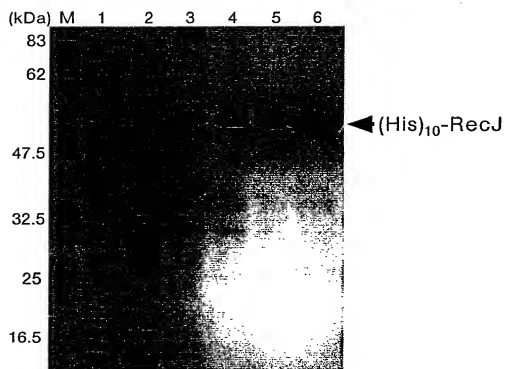


Fig.14

Motif I			
RecJ_Tt	[73]	KRIRVHGDYAGLTGTATLVRLAALG	[100]
RecJ_Ec	[73]	TRIIIVGDFAGATSTALSVLAMRSLG	[100]
RecJ_Aa	[56]	KRIIIVGDIYVIGTGTATLYRVLKLLG	[79]
RecJ_Hp	[47]	TEIIIVGDIYAGVISSATMAKFFESLN	[74]
RecJ_Hi	[67]	QKIIIVGDFAGATSTALSVLALRQLG	[90]
PPX1_Sc	[29]	TICVGNESAMSIASAITTSYCYIYN	[52]
PRUNE_Dm	[37]	HLVGNESCLLSAVSAVTAFAVYAASS	[60]
		Motif II	
RecJ_Tt	[128]	SDLITVCGITNHAELRE	[147]
RecJ_Ec	[131]	AQLITVNGISSHAGVEH	[150]
RecJ_Aa	[133]	GDFLITVNGTSAVEEIDQ	[152]
RecJ_Hp	[102]	APLLITVNGINAFEARF	[121]
RecJ_Hi	[126]	VQLLITVNGVSSFDGVAF	[145]
PPX1_Sc	[120]	ELNSYEVNNDTPKNLKNY	[139]
PRUNE_Dm	[87]	PLVCEMVCRARVALPRRY	[106]
		Motif III	
RecJ_Tt	[153]	VEVITVIRTPGK	[165]
RecJ_Ec	[155]	IPVITVIRPLGD	[165]
RecJ_Aa	[154]	LETVTIRNVPP	[164]
RecJ_Hp	[126]	YTLITIRCLHH	[136]
RecJ_Hi	[150]	IRVLTIRLPPE	[151]
PPX1_Sc	[141]	NVVGITIRFIDLQ	[153]
PRUNE_Dm	[128]	NVTILIRPLED	[140]
		Motif IV	
RecJ_Tt	[209]	YADLAAGVLTAVPLWGN	[228]
RecJ_Ec	[226]	LLDVALGELVAVVPDAN	[245]
RecJ_Aa	[215]	FLDLVALGELVAYMPVNPV	[234]
RecJ_Hp	[189]	LLCLAGVATLAMPETFF	[208]
RecJ_Hi	[219]	LLDELVALGELVAVVPDQN	[238]
PPX1_Sc	[191]	IALLMGATLITSNRRK	[210]
PRUNE_Dm	[183]	VAQLHATITVLITINEAPA	[202]
		Specific motif	
RecJ_Tt	[386]	DLLLRYIRKEAAGFAM	[402]
RecJ_Ec	[421]	GMMLKFIIRAMAAGLSL	[438]
RecJ_Aa	[404]	DMFLKNIIRDKAMGLTL	[420]
RecJ_Hp	[372]	SLLLGYIRIQACGLSV	[388]
RecJ_Hi	[415]	NMILKFIIRAMAAGLSI	[431]

Tt : *Thermus thermophilus* HB8, Ec : *Escherichia coli*, Aa : *Aquifex aeolicus*,
 Hp : *Helicobacter pylori*, Hi : *Haemophilus influenzae* Rd,
 Sc : *Saccharomyces cerevisiae*, Dm : *Drosophila melanogaster*

Fig.15

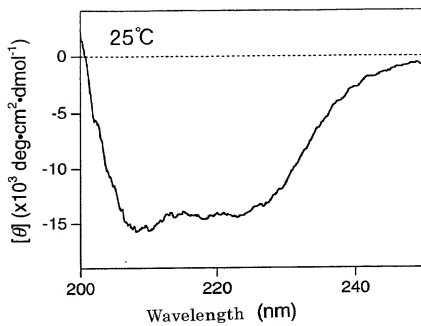


Fig.16

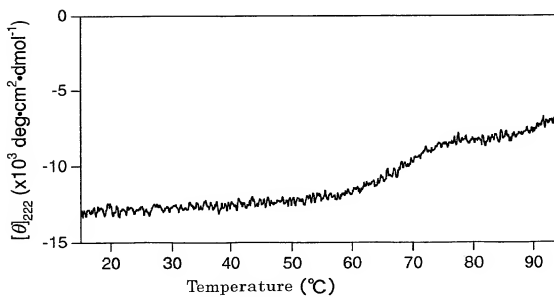


Fig.17

Substrate DNA : 49-mer ssDNA

5'-ACTACTTGGTACACTGACGCGAGCACGCAGGAGCTCATTCCAGTGCGCA-3'

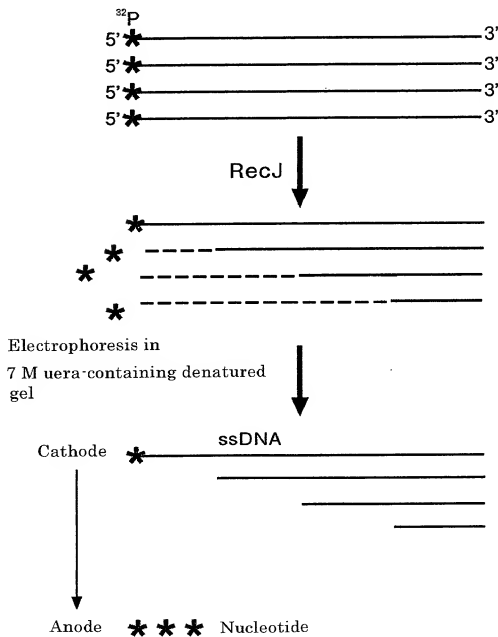


Fig.18

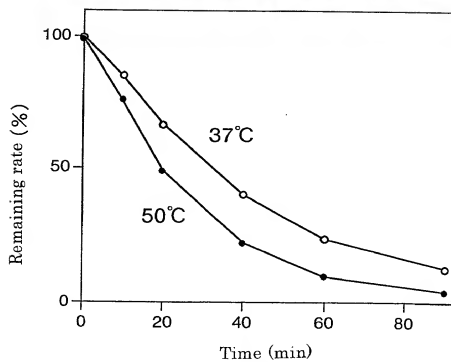
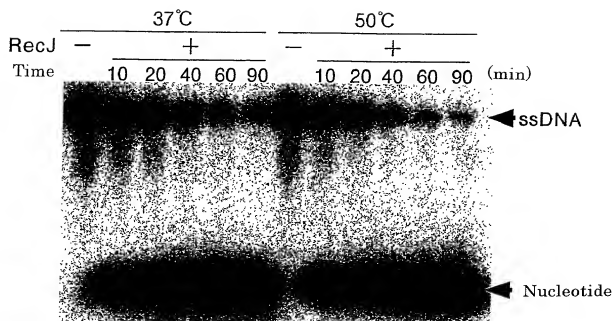


Fig.19

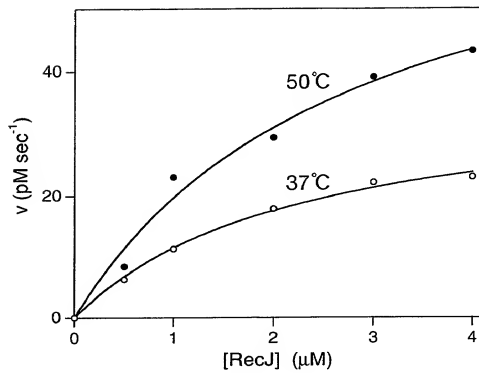


Fig.20

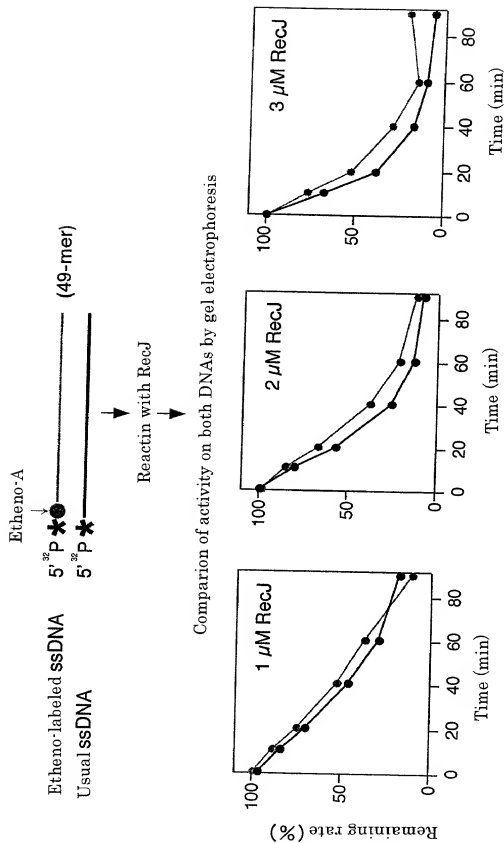
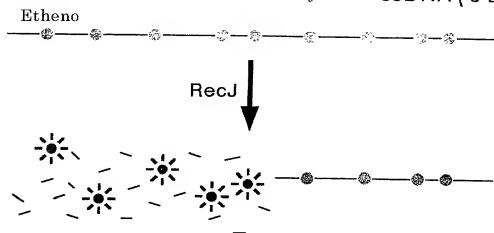


Fig.21

Substrate DNA : Etheno-labeled bovine thymus ssDNA (ϵ DNA)



Fluorescence Spectrum

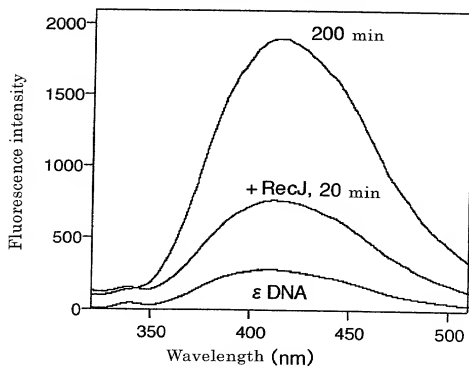


Fig.22

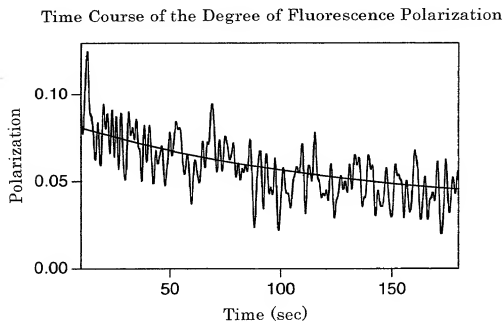
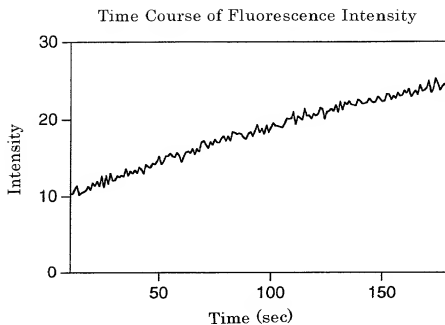


Fig.23

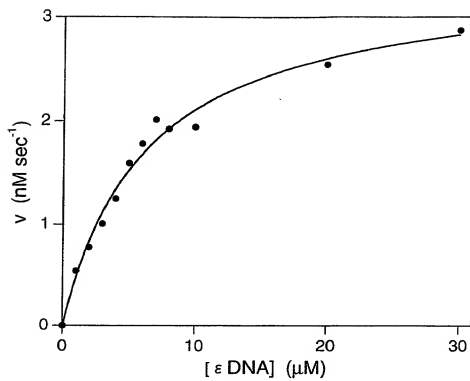


Fig.24

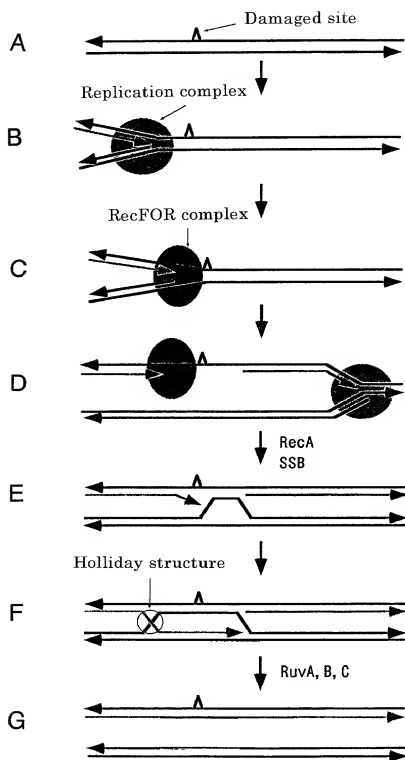


Fig.25

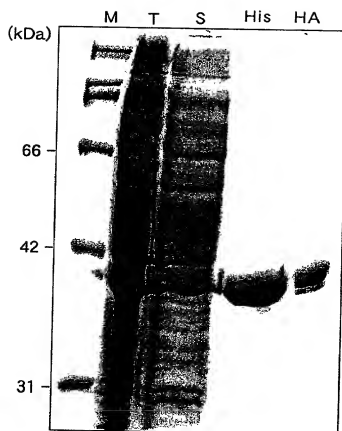


Fig.26

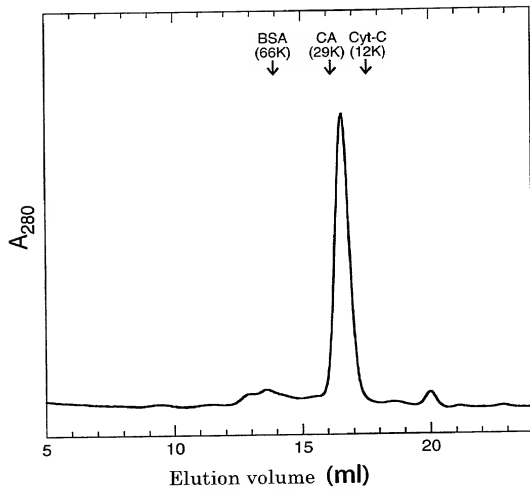


Fig.27

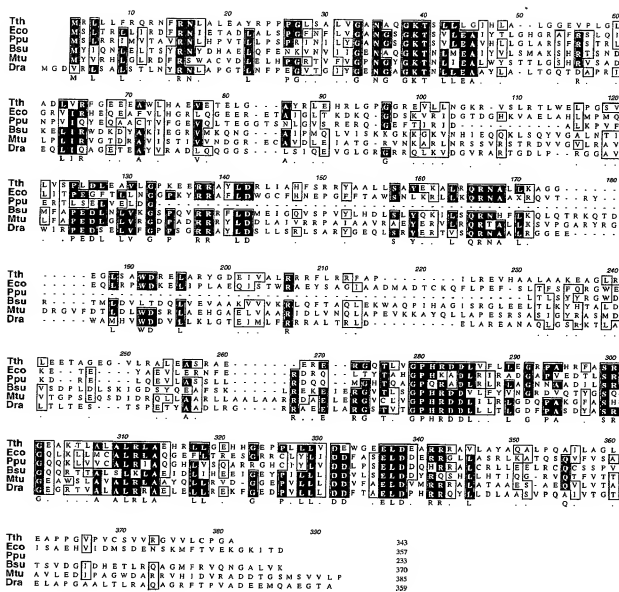
Tth: *Thermus thermophilus* HB8Eco: *Escherichia coli*Ppu: *Pseudomonas putida*Bsu: *Bacillus subtilis*Mtu: *Mycobacterium tuberculosis*Dra: *Deinococcus radiodurans*

Fig.28

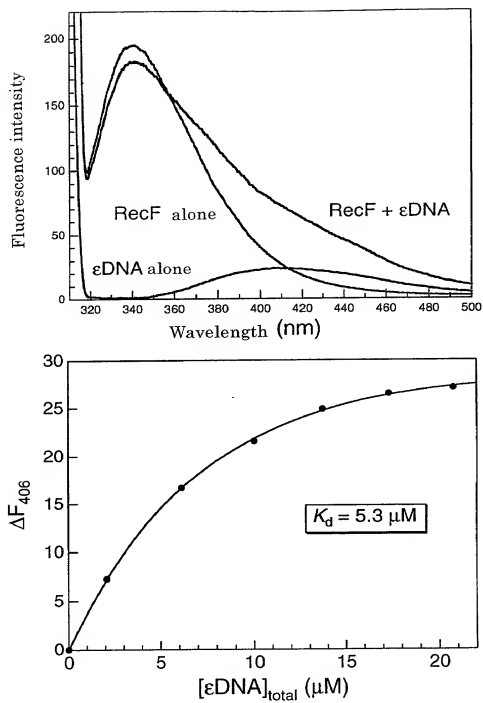


Fig.29

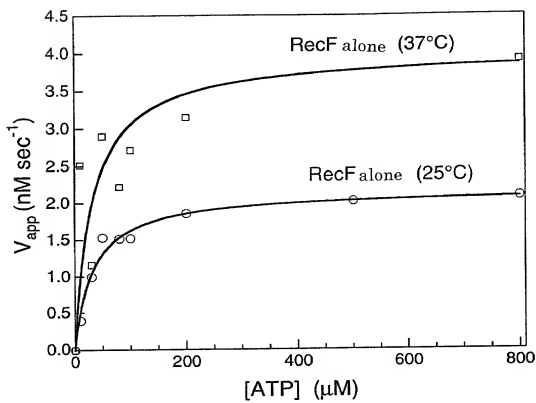


Fig.30

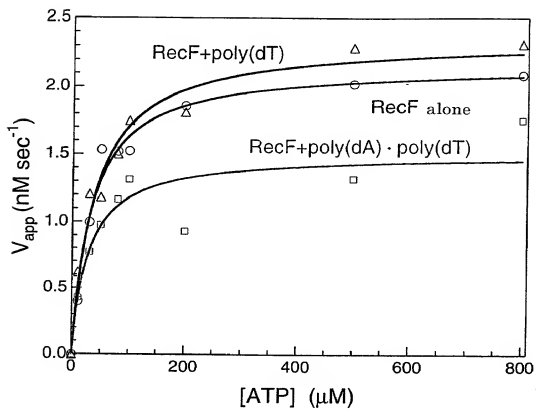


Fig.31

Repair of Entire Genome

Transcription-Coupled Repair

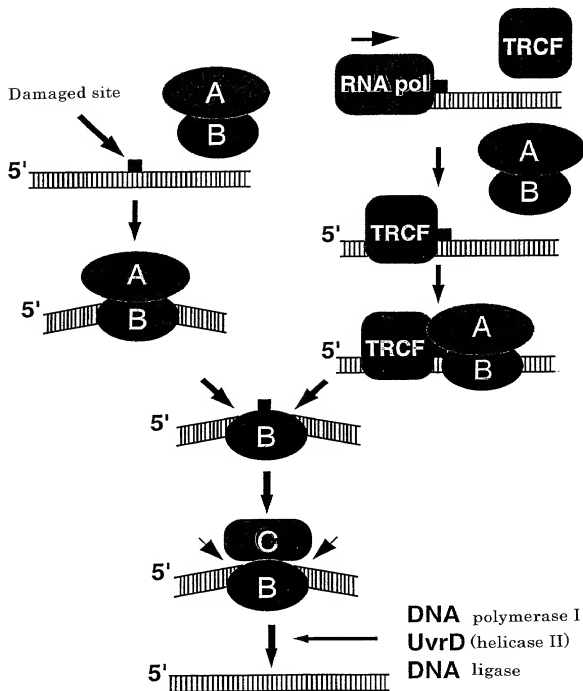


Fig.32

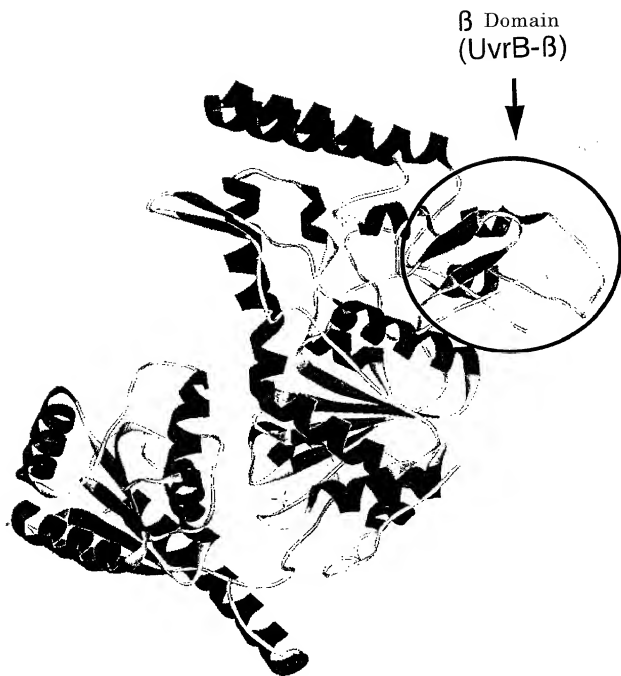
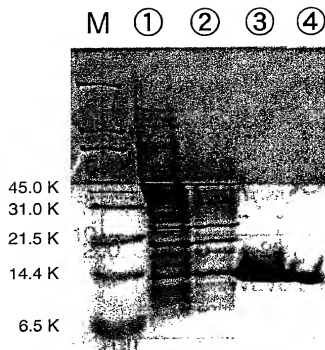


Fig.33

UvrB- β



TRCF- β

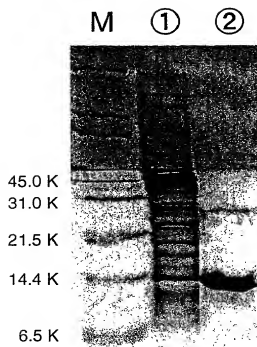


Fig.34

UvrB-β 154 RNLVVERGKPYPREVLLERLLELGYQRNDI 184
 TRCF-β 86 WRLLLEVGRAYPREALLSRLCLKGYAR--- 113
 * . * * . * * * * * * * *

UvrB-β 185 DLSGGRFRAGGEVLEIFPAYETEPTRVELF 215
 TRCF-β 114 DED---YRVLGEVVELG-----EVRLEFF 148
 * * * * * . * * *

UvrB-β 216 GDEVERISQVHPVTG-ERLRELPG----- 236
 TRCF-β 149 GDELERLVVRGEERRRHVLLPKPGKAEGFT 163
 * * * . * * *

UvrB-β 237 ---FVLFP 242 * Identical amino acid residues
 TRCF-β 164 SKKVLHEPG 172 . Homologous amino acid residues
 . **

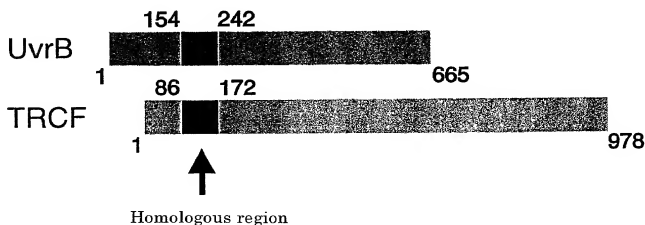


Fig.35

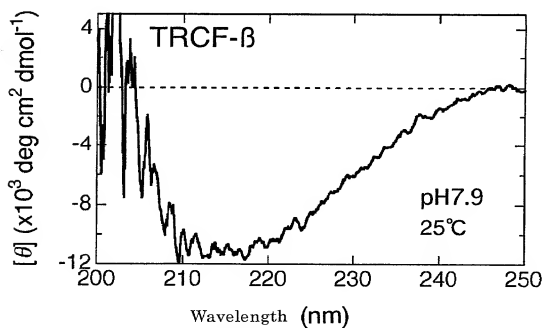
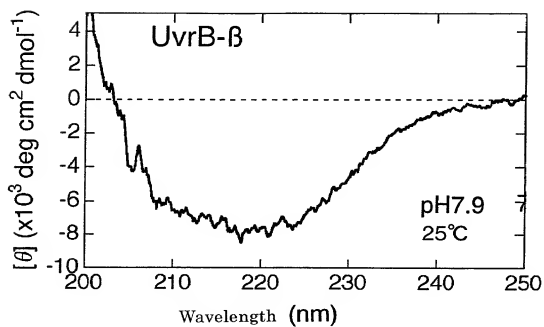


Fig.36

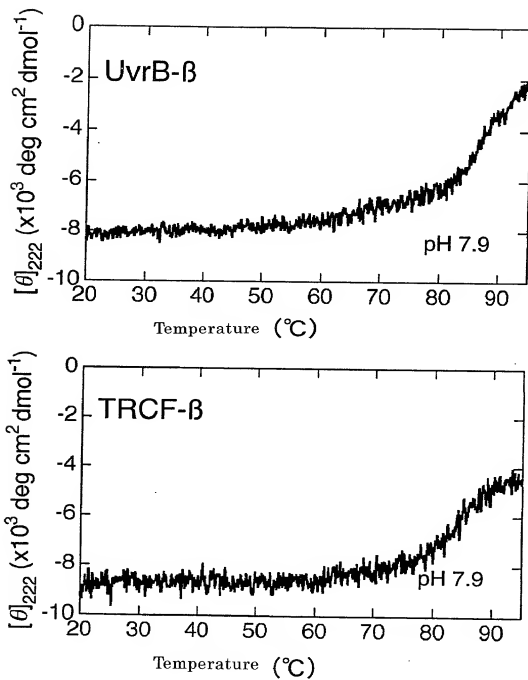


Fig.37

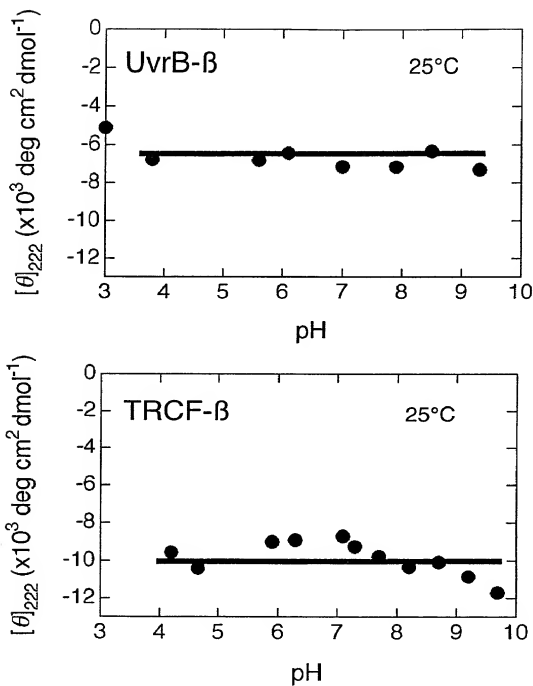


Fig.38

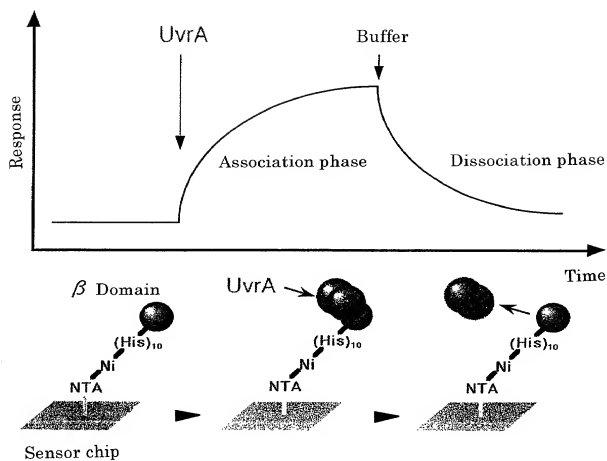
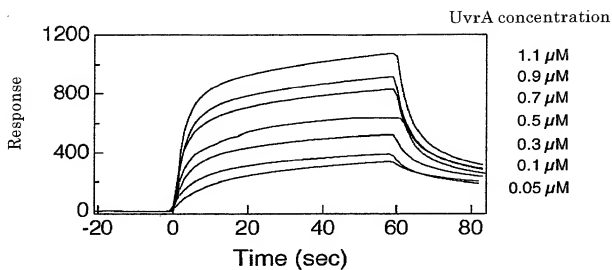


Fig.39

Sensorgram



Analytical Results

	K_d ($\times 10^{-6}$ M)		k_{on} ($\times 10^5$ M $^{-1}$ S $^{-1}$)		k_{off} ($\times 10^{-1}$ S $^{-1}$)	
	- ATP	+ ATP	- ATP	+ ATP	- ATP	+ ATP
UvrB- β	2.6	0.4	2.0	1.5	5.2	0.6
TRCF- β	1.3	0.5	1.0	1.5	1.3	0.7